



32688sequencelisting.txt

SEQUENCE LISTING

<110> Geiser, Martin  
Geisse, Sabine  
Ostemeier, Christian  
Ramage, Paul  
Raulf, Friedrich  
Zenke, Gerhard

<120> Three-Dimensional Structure of the  
Catalytic Domain of ZAP-70 Protein Tyrosine Kinase, Methods  
and Use Thereof

<130> 4-32688

<140> US 10/528,709

<141> 2005-03-22

<150> PCT/EP03/10686

<151> 2003-09-25

<150> US 60/413,704

<151> 2002-09-26

<160> 6

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 619

<212> PRT

<213> Homo sapiens

<400> 1

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 20          25          30
Leu Phe Leu Leu Arg Gln Cys Leu Arg Ser Leu Gly Gly Tyr Val Leu
 35          40          45
Ser Leu Val His Asp Val Arg Phe His His Phe Pro Ile Glu Arg Gln
 50          55          60
Leu Asn Gly Thr Tyr Ala Ile Ala Gly Gly Lys Ala His Cys Gly Pro
 65          70          75          80
Ala Glu Leu Cys Glu Phe Tyr Ser Arg Asp Pro Asp Gly Leu Pro Cys
 85          90          95
Asn Leu Arg Lys Pro Cys Asn Arg Pro Ser Gly Leu Glu Pro Gln Pro
100          105          110
Gly Val Phe Asp Cys Leu Arg Asp Ala Met Val Arg Asp Tyr Val Arg
115          120          125
Gln Thr Trp Lys Leu Glu Gly Glu Ala Leu Glu Gln Ala Ile Ile Ser
130          135          140
Gln Ala Pro Gln Val Glu Lys Leu Ile Ala Thr Thr Ala His Glu Arg
145          150          155          160
Met Pro Trp Tyr His Ser Ser Leu Thr Arg Glu Glu Ala Glu Arg Lys
165          170          175
Leu Tyr Ser Gly Ala Gln Thr Asp Gly Lys Phe Leu Leu Arg Pro Arg
180          185          190
Lys Glu Gln Gly Thr Tyr Ala Leu Ser Leu Ile Tyr Gly Lys Thr Val
195          200          205
Tyr His Tyr Leu Ile Ser Gln Asp Lys Ala Gly Lys Tyr Cys Ile Pro
210          215          220
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Glu Gly Thr Lys Phe Asp Thr Leu Trp Gln Leu Val Glu Tyr Leu Lys  
 225 230 235 240  
 Leu Lys Ala Asp Gly Leu Ile Tyr Cys Leu Lys Glu Ala Cys Pro Asn  
 245 250 255  
 Ser Ser Ala Ser Asn Ala Ser Gly Ala Ala Ala Pro Thr Leu Pro Ala  
 260 265 270  
 His Pro Ser Thr Leu Thr His Pro Gln Arg Arg Ile Asp Thr Leu Asn  
 275 280 285  
 Ser Asp Gly Tyr Thr Pro Glu Pro Ala Arg Ile Thr Ser Pro Asp Lys  
 290 295 300  
 Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr Ser  
 305 310 315 320  
 Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp Asn  
 325 330 335  
 Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser Val  
 340 345 350  
 Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala Ile  
 355 360 365  
 Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met Met  
 370 375 380  
 Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val Arg  
 385 390 395 400  
 Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu Met  
 405 410 415  
 Ala Gly Gly Gly Pro Leu His Lys Phe Leu Val Gly Lys Arg Glu Glu  
 420 425 430  
 Ile Pro Val Ser Asn Val Ala Glu Leu Leu His Gln Val Ser Met Gly  
 435 440 445  
 Met Lys Tyr Leu Glu Glu Lys Asn Phe Val His Arg Asp Leu Ala Ala  
 450 455 460  
 Arg Asn Val Leu Leu Val Asn Arg His Tyr Ala Lys Ile Ser Asp Phe  
 465 470 475 480  
 Gly Leu Ser Lys Ala Leu Gly Ala Asp Asp Ser Tyr Tyr Thr Ala Arg  
 485 490 495  
 Ser Ala Gly Lys Trp Pro Leu Lys Trp Tyr Ala Pro Glu Cys Ile Asn  
 500 505 510  
 Phe Arg Lys Phe Ser Ser Arg Ser Asp Val Trp Ser Tyr Gly Val Thr  
 515 520 525  
 Met Trp Glu Ala Leu Ser Tyr Gly Gln Lys Pro Tyr Lys Lys Met Lys  
 530 535 540  
 Gly Pro Glu Val Met Ala Phe Ile Glu Gln Gly Lys Arg Met Glu Cys  
 545 550 555 560  
 Pro Pro Glu Cys Pro Pro Glu Leu Tyr Ala Leu Met Ser Asp Cys Trp  
 565 570 575  
 Ile Tyr Lys Trp Glu Asp Arg Pro Asp Phe Leu Thr Val Glu Gln Arg  
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 Gly Ser Thr Gln Lys Ala Glu Ala Ala Cys Ala  
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<210> 2  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

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 Val Tyr Glu Ser Pro Tyr Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys  
 20 25 30  
 Leu Phe Leu Lys Arg Asp Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly

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      35      40      45
Cys Gly Asn Phe Gly Ser Val Arg Gln Gly Val Tyr Arg Met Arg Lys
 50      55      60
Lys Gln Ile Asp Val Ala Ile Lys Val Leu Lys Gln Gly Thr Glu Lys
 65      70      75      80
Ala Asp Thr Glu Glu Met Met Arg Glu Ala Gln Ile Met His Gln Leu
      85      90      95
Asp Asn Pro Tyr Ile Val Arg Leu Ile Gly Val Cys Gln Ala Glu Ala
 100      105      110
Leu Met Leu Val Met Glu Met Ala Gly Gly Gly Pro Leu His Lys Phe
 115      120      125
Leu Val Gly Lys Arg Glu Glu Ile Pro Val Ser Asn Val Ala Glu Leu
 130      135      140
Leu His Gln Val Ser Met Gly Met Lys Tyr Leu Glu Glu Lys Asn Phe
 145      150      155      160
Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Val Asn Arg His
      165      170      175
Tyr Ala Lys Ile Ser Asp Phe Gly Leu Ser Lys Ala Leu Gly Ala Asp
 180      185      190
Asp Ser Tyr Tyr Thr Ala Arg Ser Ala Gly Lys Trp Pro Leu Lys Trp
 195      200      205
Tyr Ala Pro Glu Cys Ile Asn Phe Arg Lys Phe Ser Ser Arg Ser Asp
 210      215      220
Val Trp Ser Tyr Gly Val Thr Met Trp Glu Ala Leu Ser Tyr Gly Gln
 225      230      235      240
Lys Pro Tyr Lys Lys Met Lys Gly Pro Glu Val Met Ala Phe Ile Glu
      245      250      255
Gln Gly Lys Arg Met Glu Cys Pro Pro Glu Cys Pro Pro Glu Leu Tyr
 260      265      270
Ala Leu Met Ser Asp Cys Trp Ile Tyr Lys Trp Glu Asp Arg Pro Asp
 275      280      285
Phe Leu Thr Val Glu Gln Arg Met Arg Ala Cys Tyr Tyr Ser Leu Ala
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Ser Lys Val Glu Gly Pro Pro Gly Ser Thr Gln Lys Ala Glu Ala Ala
 305      310      315      320
Cys Ala

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 <211> 20  
 <212> DNA  
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<210> 5

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